

O'Bryen, Barbara

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**From:** Switzer, Juliet  
**Sent:** Wednesday, February 09, 2005 4:05 PM  
**To:** O'Bryen, Barbara  
**Subject:** FW: please search

here's the sequence of I want searched:

aaatgctctgtrtatatgctataagc

the case is CRFE but not in ABSS b/c the CRF is too big. you'd have to go get the CD from mark spencer, but I've already OCR'd the sequence.  
thanks.

-----Original Message-----

**From:** Switzer, Juliet  
**Sent:** Wednesday, February 09, 2005 3:42 PM  
**To:** O'Bryen, Barbara  
**Subject:** please search

please search nucleotides 191-220 of seq id no 1 from 09/925065 in genseq and uspat issued and published.

results on paper is fine

thanks.

J

Juliet Switzer  
Art Unit 1634  
phone: 571-272-753  
office: Remsen 2D75

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	146	(thiopurine with methyltransferase) or tpmt	US-PGPUB; USPAT	OR	ON	2005/02/09 15:42
L2	54	l1 same (mutation polymorphism snp)	US-PGPUB; USPAT	OR	ON	2005/02/09 15:34
L3	4	l2 same intron\$3	US-PGPUB; USPAT	OR	ON	2005/02/09 15:34
L4	12	(thiopurine with methyltransferase) or tpmt	DERWENT	OR	ON	2005/02/09 15:42

(FILE 'HOME' ENTERED AT 13:36:40 ON 09 FEB 2005)

STN<sup>1</sup>

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:36:48 ON 09 FEB 2005

L1 1317 S THIOPURINE(3A)METHYLTRANSFERASE  
L2 928 S TPMT  
L3 537 S (L1 OR L2) (4A) (POLYMORPH? OR SNP OR ALLEL?)  
L4 6 S L3(6A) (INTRON?)  
L5 3 DUP REM L4 (3 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 13:40:29 ON 09 FEB 2005

L6 0 S L3 AND (ADENINE OR GUANINE)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:19:38 ON 09 FEB 2005

L7 15 S L6  
L8 12 DUP REM L7 (3 DUPLICATES REMOVED)



# results of BLAST

BLASTN 2.2.10 [Oct-19-2004]

RID: 1107966805-21412-170660323395.BLASTQ4

Blast Seq ID 1  
against dbSNP

Database: human\_snp

10,022,444 sequences; 11,321,078,719 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

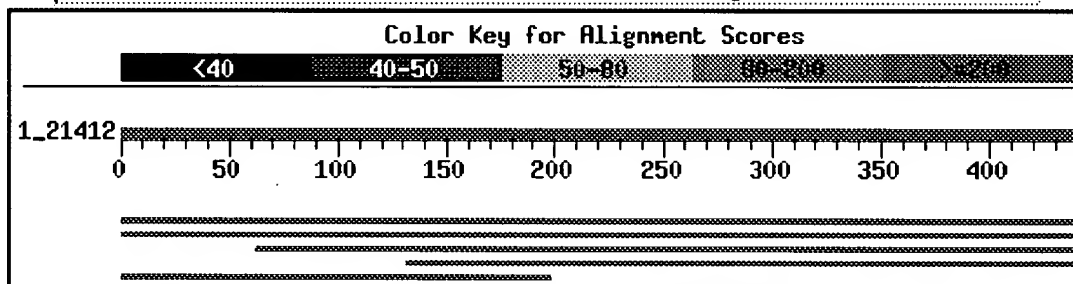
No hits in prior art.

Query=

(440 letters)

## Distribution of 5 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score E  
(bits) Value

gnl dbSNP rs3925948	allelePos=205totallen=440;taxid=9606;sn...	<u>845</u>	0.0
gnl dbSNP rs13216460	allelePos=501totallen=941;taxid=9606;s...	<u>837</u>	0.0
gnl dbSNP rs2842946	allelePos=405totallen=605;taxid=9606;sn...	<u>724</u>	0.0
gnl dbSNP rs9367980	allelePos=500totallen=1000;taxid=9606;s...	<u>587</u>	e-165
gnl dbSNP rs9465101	allelePos=151totallen=512;taxid=9606;sn...	<u>375</u>	e-101

## Alignments

>gnl|dbSNP|rs3925948 allelePos=205totallen=440;taxid=9606;snpClass=1;alleles='A/G';m  
enomic;build=111  
Length = 440

Score = 845 bits (439), Expect = 0.0  
Identities = 163/440 (37%)  
Strand = Plus / Plus

bad

bad  
date

2/9/05

bad  
date

Sbjct: 365 gtcacccaggctggagtacagaagtgcaatcacagctcactgcagcctcgacctccctgg 306

Sbjct: 305 gcacaagtgatcctcccacctcagcctcccaagtttctgggaccagaggcatgcaccaca 246

Sbjct: 245 atgcttagctaatttttc 228

```
>gnl|dbSNP|rs9367980 allelePos=500totallen=1000;taxid=9606;snpClass=1;alleles='A/C';
      nomic;build=121
      Length = 1000
```

Score = 587 bits (305), Expect = e-165  
Identities = 109/309 (35%)  
Strand = Plus / Minus

Sbjct: 1000 aaaagataaagaccattttattgaaagttgttttatcttagaaaaggaactaatctctgt 941

Sbjct: 940 aaatatgctctgtatatatgctatatgctctatgttaaaggatatttgaacttttctagaq 881

Sbjct: 880 agatgggtatatTTTTTTTTTatttgtttatttttgagataggatcttgatctgtcaccacg 821

Sbjct: 820 gctggagtacagaagtgcaatcacagctcactgcagcctcgacctccctgggcacaaagtg 761

Sbjct: 760 atcctccacctcagcctcccaagtttctgggaccagagcatgcaccacaatgcttagc 701

Sbjct: 700 taatttttc 692

```
>gnl|dbSNP|rs9465101 allelePos=151totallen=512;taxid=9606;snpClass=1;alleles='A/T';m
    enomic;build=119
```

Score = 375 bits (195), Expect = e-101  
Identities = 121/199 (60%)  
Strand = Plus / Minus

```

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 10022444
Number of Hits to DB: 6981
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 1.0e-02: 0
Number of HSP's better than 0.0 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 0.0: 0
Length of query: 440
Length of database: 11,321,078,719
Length adjustment: 25
Effective length of query: 415
Effective length of database: 11,070,517,619
Effective search space: 4594264811885
Effective search space used: 4594264811885
A: 0
X1: 13 (25.0 bits)
X2: 31 (60.0 bits)
X3: 25 (50.0 bits)
S1: 13 (25.0 bits)

```



S2: 25 (48.8 bits)